



SEQUENCE LISTING

<110> VAN HIJUM, SACHA ADRIANUS FOKKE TACO
VAN GEEL-SCHUTTEN, GERRITDINA HENDRIKA
DIJKHUIZEN, LUBBERT
RAHAOUI, HAKIM

<120> NOVEL FRUCTOSYLTRANSFERASES

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<141> 2001-11-29

<150> 09/604,958

<151> 2000-06-28

<150> EPO 00201872.9

<151> 2000-05-25

<160> 40

<170> PatentIn Ver. 2.1

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<213> Lactobacillus reuteri

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ctt gca gaa att aac aaa cgt cga ttt aac taaatactttt aaaataaaaac	2454
Leu Ala Glu Ile Asn Lys Arg Arg Phe Asn	
800 805	
cgctaagcct taaattcagc ttaacggttt tttatttttaa aagtttttat tgtaaaaaag	2514
cgaattatca ttaatactaa tgcaattggt gtaagacctt acgacagtag taacaatgaa	2574
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<213> Lactobacillus reuteri

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<213> Lactobacillus reuteri

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<210> 9

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Glu Val Glu

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 aatgtgccta ggatgcataa tggatgtaaa ttactagatg gcggttttta tacattaacc 180
 tcgcaggaga gaaaagaagc aattagtaag gatccatagc cagataaatt tattaggcct 240
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 gaattcagat cgcagcaaaa aagtaaagat acacaaaaat atgcaaaacg gcccatgcta 420
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 tcttattcac taatgctaata cccaatgct agtaatttta atttcggtat tctagaatct 600
 aaagttcact atatttggtt aaaaaacttt tgcggtcggc tgaagtccga ttatcgttat 660
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 aaaaccaata ttttataaag acagtaaag ttaatttgat aaaaacatat atttaataaa 1020
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 tgtagaaact aattcaattt gataaacggt agacatttct gaggaggaag tcattttgga 1200

gtacaaagaa cataagaaa atg tat aaa gtc ggc aag aat tgg gcc gtt gct	1252
Met Tyr Lys Val Gly Lys Asn Trp Ala Val Ala	
1 5 10	
aca ttg gta tca gct tca att tta atg gga ggg gtt gta acc gct cat	1300
Thr Leu Val Ser Ala Ser Ile Leu Met Gly Gly Val Val Thr Ala His	
15 20 25	
gct gat caa gta gaa agt aac aat tac aac ggt gtt gct gaa gtt aat	1348
Ala Asp Gln Val Glu Ser Asn Asn Tyr Asn Gly Val Ala Glu Val Asn	
30 35 40	
act gaa cgt caa gct aat ggt caa att ggc gta gat gga aaa att att	1396
Thr Glu Arg Gln Ala Asn Gly Gln Ile Gly Val Asp Gly Lys Ile Ile	
45 50 55	
agt gct aac agt aat aca acc agt ggc tcg aca aat caa gaa tca tct	1444
Ser Ala Asn Ser Asn Thr Thr Ser Gly Ser Thr Asn Gln Glu Ser Ser	
60 65 70 75	
gct act aac aat act gaa aat gct gtt gtt aat gaa agc aaa aat act	1492
Ala Thr Asn Asn Thr Glu Asn Ala Val Val Asn Glu Ser Lys Asn Thr	
80 85 90	
aac aat act gaa aat gct gtt gtt aat gaa aac aaa aat act aac aat	1540
Asn Asn Thr Glu Asn Ala Val Val Asn Glu Asn Lys Asn Thr Asn Asn	
95 100 105	
act gaa aat gct gtt gtt aat gaa aac aaa aat act aac aac aca gaa	1588
Thr Glu Asn Ala Val Val Asn Glu Asn Lys Asn Thr Asn Asn Thr Glu	
110 115 120	
aac gat aat agt caa tta aag tta act aat aat gaa caa cca tca gcc	1636
Asn Asp Asn Ser Gln Leu Lys Leu Thr Asn Asn Glu Gln Pro Ser Ala	
125 130 135	
gct act caa gca aac ttg aag aag cta aat cct caa gct gct aag gct	1684
Ala Thr Gln Ala Asn Leu Lys Lys Leu Asn Pro Gln Ala Ala Lys Ala	
140 145 150 155	
gtt caa aat gcc aag att gat gcc ggt agt tta aca gat gat caa att	1732
Val Gln Asn Ala Lys Ile Asp Ala Gly Ser Leu Thr Asp Asp Gln Ile	
160 165 170	
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Asn Glu Leu Asn Lys Ile Asn Phe Ser Lys Ser Ala Glu Lys Gly Ala	
175 180 185	
aaa ttg acc ttt aag gac tta gag ggg att ggt aat gct att gtt aag	1828
Lys Leu Thr Phe Lys Asp Leu Glu Gly Ile Gly Asn Ala Ile Val Lys	
190 195 200	
caa gat cca caa tat gct att cct tat tct aat gct aag gaa atc aag	1876
Gln Asp Pro Gln Tyr Ala Ile Pro Tyr Ser Asn Ala Lys Glu Ile Lys	
205 210 215	

aat atg cct gca aca tac act gta gat gcc caa aca ggt aag atg gct	1924
Asn Met Pro Ala Thr Tyr Thr Val Asp Ala Gln Thr Gly Lys Met Ala	
220 225 230 235	
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His Leu Asp Val Trp Asp Ser Trp Pro Val Gln Asp Pro Val Thr Gly	
240 245 250	
tat gta tct aat tac atg ggt tat caa cta gtt att gct atg atg ggt	2020
Tyr Val Ser Asn Tyr Met Gly Tyr Gln Leu Val Ile Ala Met Met Gly	
255 260 265	
att cca aat tgc cca act gga gat aat cat atc tat ctt ctt tac aac	2068
Ile Pro Asn Ser Pro Thr Gly Asp Asn His Ile Tyr Leu Leu Tyr Asn	
270 275 280	
aag tat ggt gat aat gac ttt tct cat tgg cgc aat gca ggt tca atc	2116
Lys Tyr Gly Asp Asn Asp Phe Ser His Trp Arg Asn Ala Gly Ser Ile	
285 290 295	
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Phe Gly Thr Lys Glu Thr Asn Val Phe Gln Glu Trp Ser Gly Ser Ala	
300 305 310 315	
att gta aat gat gat ggt aca att caa cta ttt ttc acc tca aat gat	2212
Ile Val Asn Asp Asp Gly Thr Ile Gln Leu Phe Phe Thr Ser Asn Asp	
320 325 330	
acg tct gat tac aag ttg aat gat caa cgc ctt gct acc gca aca tta	2260
Thr Ser Asp Tyr Lys Leu Asn Asp Gln Arg Leu Ala Thr Ala Thr Leu	
335 340 345	
aac ctt aat gtt gat gat aac ggt gtt tca atc aag agt gtt gat aat	2308
Asn Leu Asn Val Asp Asp Asn Gly Val Ser Ile Lys Ser Val Asp Asn	
350 355 360	
tat caa gtt ttg ttt gaa ggt gat gga ttt cac tac caa act tat gaa	2356
Tyr Gln Val Leu Phe Glu Gly Asp Gly Phe His Tyr Gln Thr Tyr Glu	
365 370 375	
caa ttc gca aac ggc aaa gat cgt gaa aat gat gat tac tgc tta cgt	2404
Gln Phe Ala Asn Gly Lys Asp Arg Glu Asn Asp Asp Tyr Cys Leu Arg	
380 385 390 395	
gac cca cac gtt gtt caa tta gaa aat ggt gat cgt tat ctt gta ttc	2452
Asp Pro His Val Val Gln Leu Glu Asn Gly Asp Arg Tyr Leu Val Phe	
400 405 410	
gaa gct aat act ggg aca gaa gat tac caa agt gac gac caa att tat	2500
Glu Ala Asn Thr Gly Thr Glu Asp Tyr Gln Ser Asp Asp Gln Ile Tyr	
415 420 425	
aat tgg gct aac tat ggt ggc gat gat gcc ttc aat att aag agt tcc	2548
Asn Trp Ala Asn Tyr Gly Gly Asp Asp Ala Phe Asn Ile Lys Ser Ser	
430 435 440	

ttc aag ctt ttg aat aat aag aag gat cgt gaa ttg gct ggt tta gct	2596
Phe Lys Leu Leu Asn Asn Lys Lys Asp Arg Glu Leu Ala Gly Leu Ala	
445 450 455	
aat ggt gca ctt ggt atc tta aag ctc act aac aat caa agt aag cca	2644
Asn Gly Ala Leu Gly Ile Leu Lys Leu Thr Asn Asn Gln Ser Lys Pro	
460 465 470 475	
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Lys Val Glu Glu Val Tyr Ser Pro Leu Val Ser Thr Leu Met Ala Cys	
480 485 490	
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495 500 505	
act cgt gta agt cgt ggt tcc gat cgt gaa tta acc gct aag gat aac	2788
Thr Arg Val Ser Arg Gly Ser Asp Arg Glu Leu Thr Ala Lys Asp Asn	
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Thr Ile Val Gly Asp Asn Val Ala Met Ile Gly Tyr Val Ser Asp Ser	
525 530 535	
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Leu Met Gly Lys Tyr Lys Pro Leu Asn Asn Ser Gly Val Val Leu Thr	
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Ala Ser Val Pro Ala Asn Trp Arg Thr Ala Thr Tyr Ser Tyr Ala	
560 565 570	
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Val Pro Val Ala Gly His Pro Asp Gln Val Leu Ile Thr Ser Tyr Met	
575 580 585	
agt aac aag gac ttt gct tca ggt gaa gga aac tat gca act tgg gca	3028
Ser Asn Lys Asp Phe Ala Ser Gly Glu Gly Asn Tyr Ala Thr Trp Ala	
590 595 600	
cca agt ttc tta gta caa atc aat cca gat gac acg aca act gta tta	3076
Pro Ser Phe Leu Val Gln Ile Asn Pro Asp Asp Thr Thr Thr Val Leu	
605 610 615	
gca cgt gca act aac caa ggt gac tgg gtg tgg gac gac tct agt cgg	3124
Ala Arg Ala Thr Asn Gln Gly Asp Trp Val Trp Asp Asp Ser Ser Arg	
620 625 630 635	
aac gat aat atg ctc ggt gtt ctt aaa gaa ggt gca gct aac agt gcc	3172
Asn Asp Asn Met Leu Gly Val Leu Lys Glu Gly Ala Ala Asn Ser Ala	
640 645 650	
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Ala Leu Pro Gly Glu Trp Gly Lys Pro Val Asp Trp Ser Leu Ile Asn	
655 660 665	

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Arg Ser Pro Gly Leu Gly Leu Lys Pro His Gln Pro Val Gln Pro Lys	
670 675 680	
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Ile Asp Gln Pro Asp Gln Gln Pro Ser Gly Gln Asn Thr Lys Asn Val	
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Thr Pro Gly Asn Gly Asp Lys Pro Ala Gly Lys Ala Thr Pro Asp Asn	
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act aat att gat cca agt gca caa cct tct ggt caa aac act aat att	3412
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720 725 730	
gat cca agt gca caa mct tct ggt caa aac act aag aat gtc aca cca	3460
Asp Pro Ser Ala Gln Xaa Ser Gly Gln Asn Thr Lys Asn Val Thr Pro	
735 740 745	
ggt aat gag aaa caa ggt aag aat acc gat gca aaa caa tta cca caa	3508
Gly Asn Glu Lys Gln Gly Lys Asn Thr Asp Ala Lys Gln Leu Pro Gln	
750 755 760	
aca ggt aat aag tct ggt tta gca gga ctt tac gct ggt tca tta ctt	3556
Thr Gly Asn Lys Ser Gly Leu Ala Gly Leu Tyr Ala Gly Ser Leu Leu	
765 770 775	
gcc ttg ttt gga ttg gca gca att gaa aag cgt cac gct taa	3598
Ala Leu Phe Gly Leu Ala Ala Ile Glu Lys Arg His Ala	
780 785 790	
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gattgcta	4378

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 <213> Lactobacillus reuteri

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 35 40 45
 Asn Gly Gln Ile Gly Val Asp Gly Lys Ile Ile Ser Ala Asn Ser Asn
 50 55 60
 Thr Thr Ser Gly Ser Thr Asn Gln Glu Ser Ser Ala Thr Asn Asn Thr
 65 70 75 80
 Glu Asn Ala Val Val Asn Glu Ser Lys Asn Thr Asn Asn Thr Glu Asn
 85 90 95
 Ala Val Val Asn Glu Asn Lys Asn Thr Asn Asn Thr Glu Asn Ala Val
 100 105 110
 Val Asn Glu Asn Lys Asn Thr Asn Asn Thr Glu Asn Asp Asn Ser Gln
 115 120 125
 Leu Lys Leu Thr Asn Asn Glu Gln Pro Ser Ala Ala Thr Gln Ala Asn
 130 135 140
 Leu Lys Lys Leu Asn Pro Gln Ala Ala Lys Ala Val Gln Asn Ala Lys
 145 150 155 160

Ile	Asp	Ala	Gly	Ser	Leu	Thr	Asp	Asp	Gln	Ile	Asn	Glu	Leu	Asn	Lys	165	170	175
Ile	Asn	Phe	Ser	Lys	Ser	Ala	Glu	Lys	Gly	Ala	Lys	Leu	Thr	Phe	Lys	180	185	190
Asp	Leu	Glu	Gly	Ile	Gly	Asn	Ala	Ile	Val	Lys	Gln	Asp	Pro	Gln	Tyr	195	200	205
Ala	Ile	Pro	Tyr	Ser	Asn	Ala	Lys	Glu	Ile	Lys	Asn	Met	Pro	Ala	Thr	210	215	220
Tyr	Thr	Val	Asp	Ala	Gln	Thr	Gly	Lys	Met	Ala	His	Leu	Asp	Val	Trp	225	230	235
Asp	Ser	Trp	Pro	Val	Gln	Asp	Pro	Val	Thr	Gly	Tyr	Val	Ser	Asn	Tyr	245	250	255
Met	Gly	Tyr	Gln	Leu	Val	Ile	Ala	Met	Met	Gly	Ile	Pro	Asn	Ser	Pro	260	265	270
Thr	Gly	Asp	Asn	His	Ile	Tyr	Leu	Leu	Tyr	Asn	Lys	Tyr	Gly	Asp	Asn	275	280	285
Asp	Phe	Ser	His	Trp	Arg	Asn	Ala	Gly	Ser	Ile	Phe	Gly	Thr	Lys	Glu	290	295	300
Thr	Asn	Val	Phe	Gln	Glu	Trp	Ser	Gly	Ser	Ala	Ile	Val	Asn	Asp	Asp	305	310	315
Gly	Thr	Ile	Gln	Leu	Phe	Phe	Thr	Ser	Asn	Asp	Thr	Ser	Asp	Tyr	Lys	325	330	335
Leu	Asn	Asp	Gln	Arg	Leu	Ala	Thr	Ala	Thr	Leu	Asn	Leu	Asn	Val	Asp	340	345	350
Asp	Asn	Gly	Val	Ser	Ile	Lys	Ser	Val	Asp	Asn	Tyr	Gln	Val	Leu	Phe	355	360	365
Glu	Gly	Asp	Gly	Phe	His	Tyr	Gln	Thr	Tyr	Glu	Gln	Phe	Ala	Asn	Gly	370	375	380
Lys	Asp	Arg	Glu	Asn	Asp	Asp	Tyr	Cys	Leu	Arg	Asp	Pro	His	Val	Val	385	390	395
Gln	Leu	Glu	Asn	Gly	Asp	Arg	Tyr	Leu	Val	Phe	Glu	Ala	Asn	Thr	Gly	405	410	415
Thr	Glu	Asp	Tyr	Gln	Ser	Asp	Asp	Gln	Ile	Tyr	Asn	Trp	Ala	Asn	Tyr	420	425	430
Gly	Gly	Asp	Asp	Ala	Phe	Asn	Ile	Lys	Ser	Ser	Phe	Lys	Leu	Leu	Asn	435	440	445
Asn	Lys	Lys	Asp	Arg	Glu	Leu	Ala	Gly	Leu	Ala	Asn	Gly	Ala	Leu	Gly	450	455	460

Ile	Leu	Lys	Leu	Thr	Asn	Asn	Gln	Ser	Lys	Pro	Lys	Val	Glu	Glu	Val	465	470	475	480
Tyr	Ser	Pro	Leu	Val	Ser	Thr	Leu	Met	Ala	Cys	Asp	Glu	Val	Xaa	Xaa	485	490	495	
Lys	Leu	Gly	Asp	Lys	Tyr	Tyr	Leu	Phe	Ser	Val	Thr	Arg	Val	Ser	Arg	500	505	510	
Gly	Ser	Asp	Arg	Glu	Leu	Thr	Ala	Lys	Asp	Asn	Thr	Ile	Val	Gly	Asp	515	520	525	
Asn	Val	Ala	Met	Ile	Gly	Tyr	Val	Ser	Asp	Ser	Leu	Met	Gly	Lys	Tyr	530	535	540	
Lys	Pro	Leu	Asn	Asn	Ser	Gly	Val	Val	Leu	Thr	Ala	Ser	Val	Pro	Ala	545	550	555	560
Asn	Trp	Arg	Thr	Ala	Thr	Tyr	Ser	Tyr	Tyr	Ala	Val	Pro	Val	Ala	Gly	565	570	575	
His	Pro	Asp	Gln	Val	Leu	Ile	Thr	Ser	Tyr	Met	Ser	Asn	Lys	Asp	Phe	580	585	590	
Ala	Ser	Gly	Glu	Gly	Asn	Tyr	Ala	Thr	Trp	Ala	Pro	Ser	Phe	Leu	Val	595	600	605	
Gln	Ile	Asn	Pro	Asp	Asp	Thr	Thr	Thr	Val	Leu	Ala	Arg	Ala	Thr	Asn	610	615	620	
Gln	Gly	Asp	Trp	Val	Trp	Asp	Asp	Ser	Ser	Arg	Asn	Asp	Asn	Met	Leu	625	630	635	640
Gly	Val	Leu	Lys	Glu	Gly	Ala	Ala	Asn	Ser	Ala	Ala	Leu	Pro	Gly	Glu	645	650	655	
Trp	Gly	Lys	Pro	Val	Asp	Trp	Ser	Leu	Ile	Asn	Arg	Ser	Pro	Gly	Leu	660	665	670	
Gly	Leu	Lys	Pro	His	Gln	Pro	Val	Gln	Pro	Lys	Ile	Asp	Gln	Pro	Asp	675	680	685	
Gln	Gln	Pro	Ser	Gly	Gln	Asn	Thr	Lys	Asn	Val	Thr	Pro	Gly	Asn	Gly	690	695	700	
Asp	Lys	Pro	Ala	Gly	Lys	Ala	Thr	Pro	Asp	Asn	Thr	Asn	Ile	Asp	Pro	705	710	715	720
Ser	Ala	Gln	Pro	Ser	Gly	Gln	Asn	Thr	Asn	Ile	Asp	Pro	Ser	Ala	Gln	725	730	735	
Xaa	Ser	Gly	Gln	Asn	Thr	Lys	Asn	Val	Thr	Pro	Gly	Asn	Glu	Lys	Gln	740	745	750	
Gly	Lys	Asn	Thr	Asp	Ala	Lys	Gln	Leu	Pro	Gln	Thr	Gly	Asn	Lys	Ser	755	760	765	

Gly Leu Ala Gly Leu Tyr Ala Gly Ser Leu Leu Ala Leu Phe Gly Leu
 770 775 780

Ala Ala Ile Glu Lys Arg His Ala
 785 790

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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

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24

<210> 13

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 13

catgatcata agtttggtag taatag

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<210> 14

<211> 24

<212> DNA

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<223> Description of Artificial Sequence: Primer

<400> 15

ctattactac caaacttatg atcatg

26

<210> 16

<211> 38

<212> DNA
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<220>

<223> Description of Artificial Sequence: Primer

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ccatggccat ggtagaacgc aaggacata aaaaaatg

38

<210> 17

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 17

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38

<210> 18

<211> 21

<212> DNA

<213> Artificial Sequence

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<222> (6)

<223> a, c, t, g, other or unknown

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<222> (15)

<223> a, c, t, g, other or unknown

<400> 18

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21

<210> 19

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<212> DNA

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 <222> (12)
 <223> a, c, t, g, other or unknown

<220>
 <223> Description of Artificial Sequence: Primer

<400> 19
 gtngcnswn cnswwccayts ytg

23

<210> 20
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 20
 gaatgtaggt ccaatttttg gc

22

<210> 21
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 21
 cctgtccgaa catcttgaac tg

22

<210> 22
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<220>
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<220>
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<222> (9)
 <223> a, c, t, g, other or unknown

<220>
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<220>
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 <222> (18)
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<220>
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 <222> (21)
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<400> 22
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23

<210> 23
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 <212> DNA
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<220>
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<220>
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 <222> (9)
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<220>
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<400> 23
 tayaayggng tngcngargt naa

23

<210> 24
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 24

ccgaccatct tgtttgatta ac

22

<210> 25

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 25

aaytataayg gygttgcryg aagt

24

<210> 26

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

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<223> a, c, t, g, other or unknown

<400> 26

taccgnwsnc tacttcaact t

21

<210> 27

<211> 17

<212> PRT

<213> Lactobacillus reuteri

<400> 27

Tyr Asn Gly Val Ala Glu Val Lys Lys Arg Gly Tyr Phe Tyr Ala Arg

1

5

10

15

Thr

<210> 28

<211> 17

<212> PRT

<213> Lactobacillus reuteri

<400> 28

Tyr Asn Gly Val Ala Glu Val Asn Thr Glu Arg Gln Ala Asn Gly Gly

1

5

10

15

Ile

<210> 29
 <211> 14
 <212> PRT
 <213> Bacillus amyloliquefaciens

<400> 29
 Gly Leu Asp Val Trp Asp Ser Trp Pro Leu Gln Asn Ala Asp
 1 5 10

<210> 30
 <211> 14
 <212> PRT
 <213> Bacillus subtilis

<400> 30
 Gly Leu Asp Val Trp Asp Ser Trp Pro Leu Gln Asn Ala Asp
 1 5 10

<210> 31
 <211> 14
 <212> PRT
 <213> Streptococcus mutans

<400> 31
 Asp Leu Asp Val Trp Asp Ser Trp Pro Val Gln Asp Ala Lys
 1 5 10

<210> 32
 <211> 14
 <212> PRT
 <213> Streptococcus salivarius

<400> 32
 Glu Ile Asp Val Trp Asp Ser Trp Pro Val Gln Asp Ala Lys
 1 5 10

<210> 33
 <211> 16
 <212> PRT
 <213> Bacillus amyloliquefaciens

<400> 33
 Gln Thr Gln Glu Trp Ser Gly Ser Ala Thr Phe Thr Ser Asp Gly Lys
 1 5 10 15

<210> 34
 <211> 16
 <212> PRT
 <213> Bacillus subtilis

<400> 34

Gln	Thr	Gln	Glu	Trp	Ser	Gly	Ser	Ala	Thr	Phe	Thr	Ser	Asp	Gly	Lys
1				5					10					15	

<210> 35

<211> 16

<212> PRT

<213> Streptococcus mutans

<400> 35

Leu	Thr	Gln	Glu	Trp	Ser	Gly	Ser	Ala	Thr	Val	Asn	Glu	Asp	Gly	Ser
1				5					10					15	

<210> 36

<211> 16

<212> PRT

<213> Streptococcus salivarius

<400> 36

Asp	Asp	Gln	Gln	Trp	Ser	Gly	Ser	Ala	Thr	Val	Asn	Ser	Asp	Gly	Ser
1				5					10					15	

<210> 37

<211> 11

<212> PRT

<213> Bacillus amyloliquefaciens

<400> 37

Lys	Ala	Thr	Phe	Gly	Pro	Ser	Phe	Leu	Met	Asn
1				5					10	

<210> 38

<211> 11

<212> PRT

<213> Bacillus subtilis

<400> 38

Gln	Ser	Thr	Phe	Ala	Pro	Ser	Phe	Leu	Leu	Asn
1				5					10	

<210> 39

<211> 11

<212> PRT

<213> Streptococcus mutans

<400> 39

Asn	Ser	Thr	Trp	Ala	Pro	Ser	Phe	Leu	Ile	Gln
1				5					10	

<210> 40

<211> 11

<212> PRT

<213> Streptococcus salivarius

<400> 40

Lys	Ser	Thr	Trp	Ala	Pro	Ser	Phe	Leu	Ile	Lys
1				5					10	